

## 5 SEQUENCE LISTINGS

<110> Maxygen ApS

<120> Factor VII or VIIa-like molecules

10 <130> 0212WO100

<140>

<141>

15 <160> 11

<170> PatentIn Ver. 2.1

<210> 1

20 <211> 406

<212> PRT

<213> Homo sapiens

<220>

25 <221> MOD\_RES

<222> (6)..(35)

<223> Xaa = gamma carboxyglutamic acid or glutamic acid

<400> 1

30 Ala Asn Ala Phe Leu Xaa Xaa Leu Arg Pro Gly Ser Leu Xaa Arg Xaa  
1 5 10 15

Cys Lys Xaa Xaa Gln Cys Ser Phe Xaa Xaa Ala Arg Xaa Ile Phe Lys  
20 25 30

35 Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp  
35 40 45

40 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln  
50 55 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn  
65 70 75 80

45 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly  
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys  
100 105 110

50 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr  
115 120 125

55 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg,  
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro  
145 150 155 160

5 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln  
165 170 175  
Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala  
180 185 190  
10 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu  
195 200 205  
15 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg  
210 215 220  
Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn  
225 230 235 240  
20 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp  
245 250 255  
His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr  
260 265 270  
25 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu  
275 280 285  
30 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg  
290 295 300  
Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser  
305 310 315 320  
35 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser  
325 330 335  
Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr  
340 345 350  
40 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys  
355 360 365  
45 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  
370 375 380  
Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu  
385 390 395 400  
50 Leu Arg Ala Pro Phe Pro  
405  
<210> 2  
55 <211> 1338  
<212> DNA  
<213> Homo sapiens  
<220>  
60 <221> CDS  
<222> (115) .. (1335)

5  
<400> 2  
atggtcagcc aggccctccg cctcctgtgc ctgctcctgg ggctgcaggg ctgcctggct 60

10  
gccgtcttcg tcaccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc 117  
Ala  
1

15  
aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165  
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
5 10 15

20  
aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp  
20 25 30

25  
gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261  
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln  
35 40 45

30  
tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309  
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu  
50 55 60

35  
cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc 357  
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys  
70 75 80

40  
gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc 405  
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly  
85 90 95

45  
tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc 453  
Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg  
100 105 110

50  
tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc 501  
Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro  
115 120 125

55  
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac 549  
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn  
130 135 140 145

60  
gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag 597  
Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys  
150 155 160

65  
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg 645  
Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu  
165 170 175

70  
tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac 693  
Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His  
180 185 190

75  
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc 741

5	Cys	Phe	Asp	Lys	Ile	Lys	Asn	Trp	Arg	Asn	Leu	Ile	Ala	Val	Leu	Gly	
	195						200					205					
	gaa	cac	gat	ctg	tcc	gag	cat	gac	ggg	gac	gaa	cag	tcc	cgc	cgg	gtg	789
10	Glu	His	Asp	Leu	Ser	Glu	His	Asp	Gly	Asp	Glu	Gln	Ser	Arg	Arg	Val	225
	210					215					220						
	gct	cag	gtc	atc	att	ccc	tcc	acc	tat	gtg	cct	ggc	acg	acc	aat	cac	837
	Ala	Gln	Val	Ile	Ile	Pro	Ser	Thr	Tyr	Val	Pro	Gly	Thr	Thr	Asn	His	240
15					230					235							
	gat	atc	gct	ctg	ctc	cgc	ctc	cac	cag	ccc	gtc	gtg	ctc	acc	gat	cac	885
	Asp	Ile	Ala	Leu	Leu	Arg	Leu	His	Gln	Pro	Val	Val	Leu	Thr	Asp	His	255
				245					250								
20	gtc	gtg	cct	ctg	tgc	ctg	cct	gag	cgg	acc	ttt	agc	gaa	cgc	acg	ctg	933
	Val	Val	Pro	Leu	Cys	Leu	Pro	Glu	Arg	Thr	Phe	Ser	Glu	Arg	Thr	Leu	270
			260					265					270				
	gct	ttc	gtc	cgc	ttt	agc	ctc	gtg	tcc	ggc	tgg	ggc	cag	ctg	ctc	gac	981
25	Ala	Phe	Val	Arg	Phe	Ser	Leu	Val	Ser	Gly	Trp	Gly	Gln	Leu	Leu	Asp	285
		275					280					285					
	cgg	ggc	gct	acc	gct	ctc	gag	ctg	atg	gtg	ctc	aac	gtc	ccc	cgg	ctg	1029
30	Arg	Gly	Ala	Thr	Ala	Leu	Glu	Leu	Met	Val	Leu	Asn	Val	Pro	Arg	Leu	305
	290					295					300						
	atg	acc	cag	gac	tgc	ctg	cag	cag	tcc	cgc	aaa	gtg	ggg	gac	tcc	ccc	1077
	Met	Thr	Gln	Asp	Cys	Leu	Gln	Gln	Ser	Arg	Lys	Val	Gly	Asp	Ser	Pro	320
					310					315							
35	aat	atc	acg	gag	tat	atg	ttt	tgc	gct	ggc	tat	agc	gat	ggc	tcc	aag	1125
	Asn	Ile	Thr	Glu	Tyr	Met	Phe	Cys	Ala	Gly	Tyr	Ser	Asp	Gly	Ser	Lys	335
				325				330						335			
40	gat	agc	tgc	aag	ggg	gac	tcc	ggc	ggg	ccc	cat	gcc	acg	cac	tat	cgc	1173
	Asp	Ser	Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	His	Ala	Thr	His	Tyr	Arg	350
			340					345					350				
	ggg	acc	tgg	tac	ctc	acc	ggg	atc	gtc	agc	tgg	ggc	cag	ggc	tgc	gcc	1221
45	Gly	Thr	Trp	Tyr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Gln	Gly	Cys	Ala	365
			355				360					365					
	acg	gtg	ggg	cac	ttt	ggc	gtc	tac	acg	cgc	gtc	agc	cag	tac	att	gag	1269
50	Thr	Val	Gly	His	Phe	Gly	Val	Tyr	Thr	Arg	Val	Ser	Gln	Tyr	Ile	Glu	385
	370					375					380						
	tgg	ctg	cag	aag	ctc	atg	cgg	agc	gaa	ccc	cgg	ccc	ggg	gtg	ctc	ctg	1317
	Trp	Leu	Gln	Lys	Leu	Met	Arg	Ser	Glu	Pro	Arg	Pro	Gly	Val	Leu	Leu	400
					390					395							
55	cgg	gcc	cct	ttc	cct	tga	taa										1338
	Arg	Ala	Pro	Phe	Pro												405
					405												
60	<210> 3																

5 <211> 406  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 3  
 10 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu  
     1                    5                    10                    15  
     Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys  
                     20                    25                    30  
 15 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp  
                     35                    40                    45  
     Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln  
                     50                    55                    60  
     Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn  
                     65                    70                    75                    80  
 20 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly  
                     85                    90                    95  
     Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys  
                     100                    105                    110  
     Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr  
                     115                    120                    125  
 25 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg  
                     130                    135                    140  
     Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro  
                     145                    150                    155                    160  
 30 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln  
                     165                    170                    175  
     Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala  
                     180                    185                    190  
     His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu  
                     195                    200                    205  
 35 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg  
                     210                    215                    220  
     Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn  
                     225                    230                    235                    240  
 40 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp  
                     245                    250                    255  
     His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr  
                     260                    265                    270  
 45 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu  
                     275                    280                    285  
     Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg  
                     290                    295                    300  
     Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser  
                     305                    310                    315                    320  
 50 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser  
                     325                    330                    335  
     Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr  
                     340                    345                    350  
     Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys  
                     355                    360                    365  
 55 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  
                     370                    375                    380  
     Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu  
                     385                    390                    395                    400  
 60 Leu Arg Ala Pro Phe Pro  
                     405

5

<210> 4  
 <211> 1357  
 10 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Expression  
 15 cassette for expression of FVII in mammalian cells

<400> 4  
 ggatccccgcc accatgggtca gccaggccct ccgcctcctg tgcctgctcc tggggctgca 60  
 gggctgcctg gctgccgtct tcgtcaccca ggaggaagcc catggcgctcc tgcacgcgcg 120  
 20 gcgcggggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa 180  
 agaggaacag tgcagctttg aggaagcccg ggagattttc aaagacgctg agcggaccaa 240  
 actgtttttg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg 300  
 gggctcctgc aaagaccagc tgcagagcta tatctgcttc tgctgcctg cctttgaggg 360  
 gcgcaattgc gaaacccata aggatgacca gctgatttgc gtcaacgaaa acgggggctg 420  
 25 cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctgcc acgaaggcta 480  
 tagcctcctg gctgacgggg tgtcctgcac gccacgggtg gaataccctt gcgggaagat 540  
 tcccattcta gaaaagcgga acgctagcaa accccagggc cggatcgctc gcgggaaggt 600  
 ctgccctaag ggggagtgcc cctggcaggt cctgctcctg gtcaacgggg cccagctgtg 660  
 cggcggggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat 720  
 30 taagaattgg cggaacctca tcgctgtgct cggcgaacac gatctgtccg agcatgacgg 780  
 ggacgaacag tcccgccggg tggctcaggt catcattccc tccacctatg tgctgggcac 840  
 gaccaatcac gatatcgctc tgctccgect ccaccagccc gtcgtgctca ccgatcacgt 900  
 cgtgcctctg tgctgcctg agcggacctt tagcgaacgc acgctggctt tcgtccgctt 960  
 tagcctcgtg tccggctggg gccagctgct cgaccggggc gctaccgctc tcgagctgat 1020  
 35 ggtgtcaac gtcccccggc tgatgacca ggactgcctg cagcagtccc gcaaagtggg 1080  
 ggactcccc aatatcacgg agtatatgtt ttgcgtggc tatagcgatg gctccaagga 1140  
 tagctgcaag ggggactccg gcgggcccc tgccacgcac tatcgcgga cctggtacct 1200  
 caccgggatc gtcagctggg gccagggctg cgccacgggt gggcactttg gcgtctacac 1260  
 gcgcgtcagc cagtacattg agtggctgca gaagctcatg cggagcgaac cccggcccgg 1320  
 40 ggtgctcctg cgggcccctt tcccttgata aaagctt 1357

<210> 5  
 <211> 31  
 45 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer  
 50 CBProFpr174

<400> 5  
 agctggctag ccactgggca ggtaagtatc a 31

55

<210> 6  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

60

<220>

5 <223> Description of Artificial Sequence: Primer  
CBProFpr175

<400> 6  
tggcgggatc cttaagagct gtaattgaac t 31

10

<210> 7  
<211> 30  
<212> DNA  
15 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
CBProFpr216

20

<400> 7  
cttaaggatc ccgccaccat ggtcagccag 30

25

<210> 8  
<211> 28  
<212> DNA  
<213> Artificial Sequence

30

<220>  
<223> Description of Artificial Sequence: Primer  
CBProFpr229

35

<400> 8  
ggagtccccg gttttgttgg actgctgc 28

40

<210> 9  
<211> 21  
<212> DNA  
<213> Artificial Sequence

45

<220>  
<223> Description of Artificial Sequence: Primer  
CBProFpr221

<400> 9  
acttaagctt ttatcaaggg a 21

50

<210> 10  
<211> 28  
<212> DNA  
<213> Artificial Sequence

55

<220>  
<223> Description of Artificial Sequence: Primer  
CBProFpr228

60

<400> 10  
gcagcagtcc aacaaaaccg gggactcc 28

10 <213> Artificial Sequence

15

30

$$\begin{array}{ccccccc} \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} & \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} & \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} & \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} & \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} & \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} & \left\{ \begin{array}{c} \text{C}_{10}^{\text{H}_{16}} \\ \text{C}_{10}^{\text{H}_{14}} \\ \text{C}_{10}^{\text{H}_{12}} \end{array} \right\} \\ \text{C}_{10}^{\text{H}_{16}} & \text{C}_{10}^{\text{H}_{14}} & \text{C}_{10}^{\text{H}_{12}} & \text{C}_{10}^{\text{H}_{10}} & \text{C}_{10}^{\text{H}_{8}} & \text{C}_{10}^{\text{H}_{6}} & \text{C}_{10}^{\text{H}_{4}} \end{array}$$